International Journal of Animal and Veterinary Advances 4(2): 84-92, 2012
ISSN: 2041-2908

Submitted: December 20, 2011 Accepted: January 26, 2012 Published: April 20, 2012

Population Differentiation in Dromedarian Camel: A Comparative Study of Camel Inhabiting Extremes of Geographical Distribution

Priyanka Banerjee, Jyoti Joshi, Upasna Sharma and Ramesh Kumar Vijh
National Bureau of Animal Genetic Resources, Karnal, Haryana, India

Abstract: The camel has not been subject to selective pressures and is not differentiated. The present study was undertaken to evaluate differentiation of camels inhabiting the extreme geographical habitats for the species. In this paper we compared the camel populations of India and Southern region of Africa to adjudge the differentiation between the two populations. Utilizing 12 microsatellite loci it has been demonstrated that the populations i.e., of India and South Africa are very well differentiated. The camel population of India shows differentiation among themselves owing to selection pressure and breeding for specific economic traits/parameters like carting, baggage, riding etc. The differentiation among the two camel populations was 23% while that of among population, within the two groups was 11%. A small group of Bactrian camel exhibited closeness to hill camels. Based on the published literature and in the present study it is evident that there is a general trend of increased population differentiation from South region of Africa to Indian subcontinent with India having highly differentiated populations.

Key words: FST, genetic differentiation, Indian camel, South African camel

INTRODUCTION

Camel known as a beast of burden in the desert is presently being transformed into a multiutility animal providing draft power, patrolling international borders, production of commodities like hair, meat and milk. The camel are categorized into two distinctive types, the dromedarian (C*amelus dromedarius*) and bactrian (*Camelus bactrianus*). The habitats of these two camels are distinct. Dromedarian inhabits the hot deserts of India, Pakistan, low lands of Afghanistan, Arabian Peninsula, Somalia to South and Western parts of Africa. The two humped bactrian camel is distributed in Mongolia and China but a small population of bactrian camel exists in Nubra valley of Jammu and Kashmir. Low level of population differentiation among the camels in several studies (Nolte, 2005; Saitou and Nei, 1987; Vijh *et al*., 2007) is primarily because of non-selection of camels for specific traits of economic importance. Recently, there have been several studies on camel population across continents: Australia (Spencer and Woolnough, 2010), Canarian camel and its relationship with breeds/ populations of Arab, Kenya, Pakistan and Algerian camels (Schulz, 2010), Kenyan population (MBuru *et al*., 2003) South African camel (Nolte, 2005), Majorero camel (Schulz *et al*., 2005), Indian camel (Vijh *et al*., 2007), Tunisian camel (Ahmed *et al*., 2010) and Saudi Arabian camel (Al-Swailem *et al*., 2009). All the studies have shown little differentiation (Spencer and Woolnough, 2010) among the breeds and populations except in India where the hill type camel could be differentiated from low land camel (Vijh *et al*., 2007). A comprehensive study was carried out on Canarian camel (Schulz, 2010) which included data on Arabian, Kenyan, Pakistani, UAE and Algerian camel.

India owns 0.516 million camel and is in East of Pakistan and has six defined populations of camel based on their morphological attributes. A small population of camel exists in South Africa, Nambia and Botswana and has been studied based on microsatellite markers (Nolte, 2005). These camels have their origin from North Africa (Nolte, 2005). In this present study, we have included the data on 12 microsatellites loci (Nolte, 2005) for a detailed analysis and generated data on the same loci on 798 dromedarians. We have also generated data on 17 bactrian camel and included in the present study as an out-group. The purpose of the study was to analyze the two extreme areas of dromedrian habitation-India and three countries of Southern most part of Africa utilizing data generated by (Nolte, 2005).

MATERIALS AND METHODS

The present study was undertaken in Indian camel utilizing 12 microsatellite loci on which data was generated. The data on South African camel for these 12

Coressponding author: Ramesh Kumar Vijh, National Bureau of Animal Genetic Resources, Karnal, Haryana, India

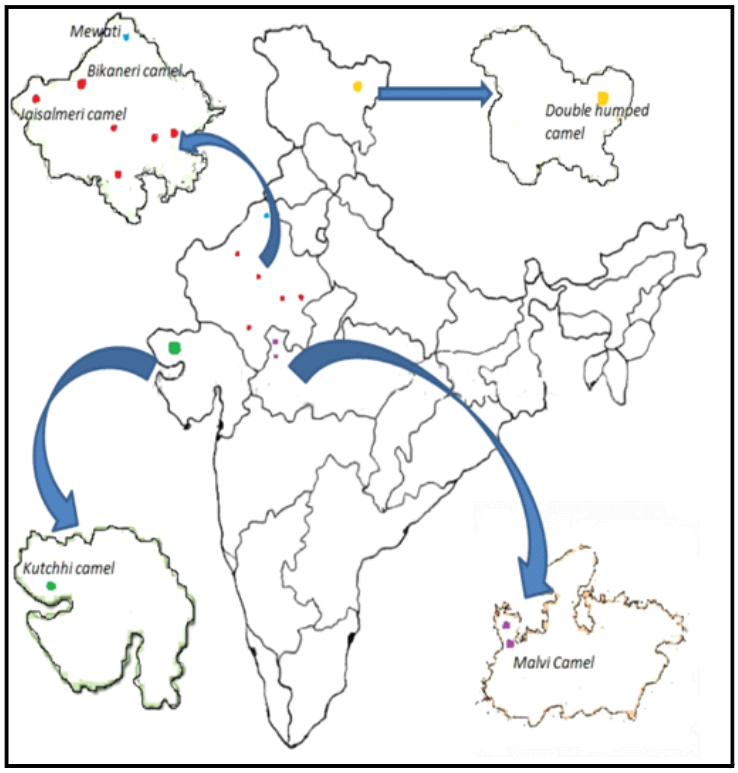

Fig. 1: Map of India showing distribution of camel in India

Table 1: List of primers

S.No.	Marker	Primer forward	Primer reverse	Dyes	Min size	Max size	Acession number	No. of alleles recorded	Type of repeats
1	LCA63	TTACCCAgTC CTTCgTggg	ggAACCTCgTgg TTATggAA	VIC	184	226	AF091123	14	$(GT)_8$ $(GC)_4$ AC $(GT)_8$
2	VOLP08	CCATTCACCCC ATCTCTC	TCgCCAgTgACCT TATTTAgA	FAM	142	148	AF305230	4	$(TG)_{10}TCCG(TG)_2$ $TCCG(TG)_5$
3	VOLP10	CTTTCTCCTTT CCTCCCTACT	CgTCCACTTC CTTCATTTC	HEX	242	268	AF305231	11	$(TG)_2$ $TA(TG)_7$ TA (TG)
4	YWLL44	CTCAACAATgC TagACCTTgg	gAgAACACAg gCTggTgAATA	FAM	101	111	GU723276	6	AC/TG repeats
5	LCA66	gTgCAgCgTCC AAATAgTCA	CCAgCATCgTC CAgTATTCA	FAM	232	246	AF091125		$(CA)_{13}$
6	VOLP67	TTAgAgggTCTA TCCAgTTTC	TggACCTAAA AgAgTggAC	HEX	144	180	AF305237	15	$(TG)_5(G)_4(TG)_9CG(TG)_7$
7	YWLL08	ATCAAgTTTgA ggTgCTTTCC	CCATggCATTg TgTTgAAgAC	FAM	110	178	Not available	25	
8	YWLL38	ggCCTAAATCC TACTAgAC	CCTCTCACTCTT gTTCTCCTC	HEX	175	189	Not available	8	
9	VOLP03	AgACggTTggg AaggTggTAA	CgACAgCAAgg CACAggA	HEX	148	168	AF305228	2	$(TG)_{13}$
10	VOLP32	ggAATggCTTgA AaggAATg	CgAGCACCTGAA AgAAgACC	FAM	183	223	AF305234	24	$(TG)_{20}$
11	LCA37	TAATTACCTC CCCCACCACA	TggACCCAggA CTTgAAATg	HEX	143	183	AF060105	8	$(CA)_8$
12	LCA77	gAgCCTTTTCT TCTTTCTCACg	gggCAAgAgAg ACTgACTgg	PET	206	246	AF091129	6	$(GT)_3A(TG)_8$

loci was utilized from earlier published work (Nolte, 2005). The blood samples (6-8 mL) from 10 bactrian camels of Nubra valley of Ladakh and 7 samples from Jammu and Kashmir Government Livestock farm at Leh were collected. The blood samples were also collected from different districts of Rajasthan viz: 40 samples were collected from Mewar district of Rajasthan, 24 of Mewati camels, 186 samples from Bikaner and 236 from Jaisalmer district of Rajasthan. 174 samples of Kutchhi camels were also collected from Rann of Kutchh area of Gujarat and 138 samples of Malvi camels were collected from Nimuch and Mandsaur districts of Madhya Pradesh (Fig. 1). The blood samples were collected using EDTA-coated vacutainer tubes (Becton Dickinson, USA). The

genomic DNA was isolated following the standard protocol involving Proteinase K digestion and phenol chloroform extraction (Sambrook and Russell, 2001). The set of primers for polymerase chain reaction (PCR) amplification of microsatellite loci were synthesized from Applied Biosystems and the forward primers were labeled with different fluorescent dyes as given in the Table 1. The PCR amplification was carried out in 25 µl reaction volume consisting of 50 ng genomic DNA, 1.5mM $MgCl_2$, 200 mM dNTPs, 5 pmol of each primer, and 1 U of Taq polymerase. The PCR reaction was carried out in Eppendorf PCRs. The thermocycling conditions utilized were initial denaturation at 95ºC for 5 min, followed by 30 cycles of 45 s at 94ºC, 45 s at annealing temperature and 1 min at 72ºC. The final extension at 72ºC was prolonged for 10 min. The samples were analyzed using Avant 3130×l Automated DNA Sequencer (Applied Biosystems) with Liz 500 as internal lane standard. The data was collected and analyzed using GeneMapper (Ver 4.1.) software (Applied Biosystems). All these processes were carried out in Comparative Genomics Lab, NBAGR, Karnal.

The microsatellite data generated was analysed to calculate the heterozygosity, number of alleles and effective number of alleles using POPGENE 1.21 (Yeh *et al*., 1999). The Hardy Weinberg Equilibrium was done using Arlequin software version 3.5 using Permutation test with forecasted chain length of 1000000 and 100000 dememorisation step. The hierarchical analysis of Molecular variance (AMOVA) was carried out using Arlequin software version 3.5 (Excoffier and Lischer, 2010). The allelic pattern showing number of alleles at various frequencies was generated using GenAlEx version 6.4 (Peakall and Smouse, 2006). The multivariate correspondence analysis was carried out using GENETIX software version 4.0 (Belkhir *et al*., 2004). The model based clusters were estimated using the STRUCTURE software version 2.3 (Pritchard, 2009). The genetic distances among different populations were calculated using software POPULATIONS version 1.2.31 (Langella, 1999). The tree was constructed using Neighbour-Joining algorithm (Saitou and Nei, 1987). The interindividual genetic distances were visualized using software FIGTREE v1.3.1 (Rambaut, 2010).

RESULTS

The microsatellite polymorphism revealed a total of 247 alleles across the two dromedarian populations and one bactrian camel population (out-group). A total of 6.5 alleles were observed in African population with a mean of 5.42 alleles per locus. In Indian dromedary the total number of alleles observed for 12 loci were 217 with an average of 18.08 alleles per locus. The total number of alleles in the bactrian camel for all these 12 loci were 84 with mean value of 7 alleles per locus. The effective number of alleles in African, Indian dromedary and Bactrian camel were 2.42, 6.06 and 4.21, respectively alleles per locus respectively. The Indian dromedarian population thus has a large number of alleles with more than one third the alleles at high frequency. The population wise number of alleles (Na) and effective number of alleles (Ne) have been depicted in table and graphically represented in Fig. 2.

The mean numbers of alleles were 4.08, 3.41 and 4.42, respectively in Botswana, Namibia and South African camel populations. The mean numbers of alleles were 10.5, 6.17, 6.17, 11.33, 11.83 and 11.50 for Malvi, Mewari, Mewati, Bikaneri, Jaisalmeri and Kutchi camel, respectively which were significantly higher than African camels. The numbers of alleles were much higher for Bikaneri, Jaisalmeri and Kutchi camel which are lowland

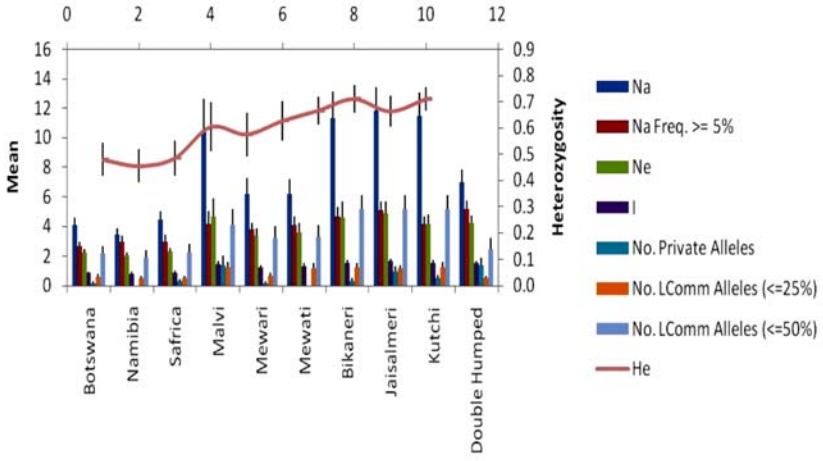

Fig. 2: Graph depicting population wise number of alleles and effective number of alleles

Table 2: Table showing observed and effective number of alleles, observed and expected heterozygosity in all the populations

Population	Na	Ne	Obs. het	He	F_{IS} value
Botswana	4.083±0.468	2.248±0.264	0.386±0.276 (75)	0.479±0.064	0.143
Namibia	3.417±0.452	2.054±0.18	0.383±0.181 (38)	0.455±0.063	0.255
Safrica	4.417±0.596	2.303±0.278	0.340±0.218 (122)	0.484±0.069	0.313
Malvi	10.5±2.116	4.679±1.231	0.626 ±0.242 (138)	0.604±0.094	0.138
Mewari	6.167±1.093	3.346±0.522	0.561±0.249 (40)	0.576±0.084	0.098
Mewati	6.167±1.058	3.593±0.606	0.591±0.258 (24)	0.627±0.075	0.157
Bikaneri	11.333±1.827	4.61±1.057	0.372±0.229 (186)	0.667±0.054	0.466
Jaiselmeri	11.833±1.628	4.867±0.809	0.389±0.188 (236)	0.711±0.055	0.483
Kutchi	11.5±1.555	4.138±0.629	0.440±0.195 (174)	0.664±0.059	0.368
Dblhump	7±0.816	4.214±0.496	0.515±0.293 (17)	0.711±0.044	0.286

Na: Number of Observed alleles; Ne: Effective number of alleles; Obs. Het: Observed Heterozygosity; He: Expected Heterozygosity; ( ): Number of individuals

Table 3: Locus wise observed and expected heterozygosity in all the 10 populations

	African camel						Indian camel			
	Botswana		Namibia		S. Africa		Malvi		Mewari	
Locus	Obs Het	Exp Het	Obs Het	Exp Het	Obs Het	Exp Het	Obs Het	Exp Het	Obs Het	Exp Het
1	0.588*	0.539	0.568	0.635	0.471*	0.678	0.5570*	0.783	0.800	0.809
2	0.352*	0.593	0.263*	0.626	0.272*	0.600	0.8760*	0.934	0.475*	0.870
3	0.435	0.441	0.324	0.471	0.415*	0.594	0.9058*	0.593	0.570*	0.758
4	0.014*	0.071	0*	0.016						
5	0*	0.511	0.236*	0.507	0.132*	0.541	0.78261*	0.786	0.075	0.073
6	0.473	0.480	0.395	0.380	0.459	0.514			0.45*	0.655
7	0*	0.139	0.000	0.052	0*	0.095	0.60870*	0.750	0.275	0.415
8	0.388*	0.720	0.526	0.629	0.655*	0.785	0.94203*	0.919	0.850	0.771
9	0.643	0.652	0.421	0.473	0.421*	0.640	0.50725*	0.782	0.725	0.703
10	0.779	0.642	0.632	0.655	0.545	0.574	0.31884*	0.638	0.800	0.741
11	0.243	0.243	0.324*	0.492	0.182	0.228	0.26515*	0.302	0.400	0.411
12	0.716	0.757	0.526	0.615	0.529	0.572	0.49275*	0.791	0.750	0.796
	Indian camel									
	Mewati		Bikaneri		Jaisalmeri		Kutchhi		Double humped	
Locus	Obs Het	Exp Het	Obs Het	Exp Het	Obs Het	Exp Het	Obs Het	Exp Het	Obs Het	Exp Het
1	0.66700	0.816	0.32796*	0.805	0.38983*	0.831	0.22414*	0.820	0.82400	0.813
2	0.70833*	0.900	0.20968*	0.690	0.36017*	0.838	0.41379*	0.836	0.70588*	0.857
3	0.91667*	0.670	0.35676*	0.573	0.56596*	0.782	0.27011*	0.461	0.35294*	0.663
4	0.45833*	0.609	0.01613*	0.514	0.19574*	0.762	0.56897*	0.731	0.00000*	0.570
5	0.75000	0.744	0.09677*	0.407	0.08584*	0.355	0.08621*	0.283	0.37500*	0.718
6			0.42900	0.467	0.47700	0.396	0.54500	0.474	0.20000*	0.363
7	0.70800	0.735	0.51892*	0.894	0.26609*	0.859	0.52874*	0.856	0.76471*	0.841
8	0.66667*	0.809	0.68817*	0.929	0.54237*	0.916	0.61494*	0.846	1.00000	0.831
9	0.54167*	0.781	0.47312*	0.795	0.54701*	0.824	0.57471*	0.811	0.37501*	0.774
10	0.29167*	0.621	0.42473*	0.667	0.48729*	0.665	0.40230*	0.581	0.41176*	0.629
11	0.0000*	0.223	0.15054*	0.435	0.09821*	0.513	0.28743*	0.447	0.41176*	0.863
12	0.7920	0.778	0.77419*	0.854	0.63983*	0.813	0.77457*	0.854	0.76471*	0.877

*: Represents significant differences between observed and expected heterozygosities ($p<0.01$)

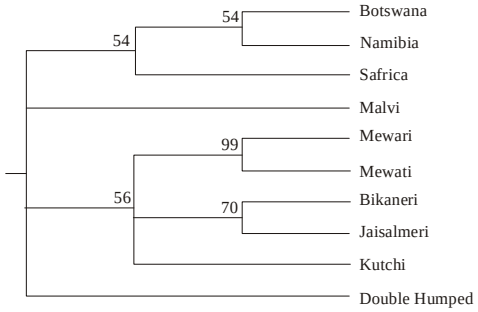

Fig. 3: Topology tree using Nei's standard genetic distance and UPGMA algorithm for tree construction

camels while the hill camel (Malvi, Mewati and Mewari) and double humped camel had significantly less number of alleles which may be due to small sample sizes taken in this study. The observed heterozygosity is low for all the three populations of South African camel (Table 2). The observed heterozygosity (Ho) is significantly high in case of Malvi, Mewari and Mewati camel breeds but low in Bikaneri and Jaisalmeri camel despite large number of camels sampled from their breeding tract. The Hardy-Weinberg Equilibrium was tested with forecasted chain length of 1000000 steps and 100000 dememorisation steps using Arelequin software v 3.5. In case of camels of Botswana , Namibia and South Africa: 6, 3, 8 out of 12

Table 4: Depicting FST (below diagonal) and nei's genetic distance (above diagonal)

	Botswana	Namibia	Safrica	Malvi	Mewari	Mewati	Bikaneri	Jaisalmeri	Kutchi	Double humped
Botswana	0.000	0.115	0.079	2.545	1.166	2.486	1.859	1.586	2.093	1.759
Namibia	0.050	0.000	0.085	2.375	1.101	2.396	1.795	1.628	2.023	1.805
Safrica	0.031	0.038	0.000	2.175	1.107	2.204	1.662	1.438	1.868	1.766
Malvi	0.327	0.333	0.320	0.000	1.747	0.163	0.815	0.961	0.675	1.338
Mewari	0.234	0.253	0.226	0.275	0.000	1.859	0.794	0.826	1.093	1.267
Mewati	0.301	0.306	0.295	0.120	0.253	0.000	0.933	0.963	0.713	1.380
Bikaneri	0.254	0.259	0.245	0.173	0.167	0.173	0.000	0.150	0.340	1.499
Jaisalmeri	0.223	0.234	0.216	0.177	0.156	0.167	0.028	0.000	0.246	1.551
Kutchi	0.259	0.265	0.250	0.155	0.189	0.149	0.068	0.048	0.000	1.505
Double Humped	0.224	0.236	0.223	0.199	0.174	0.185	0.156	0.146	0.158	0.000

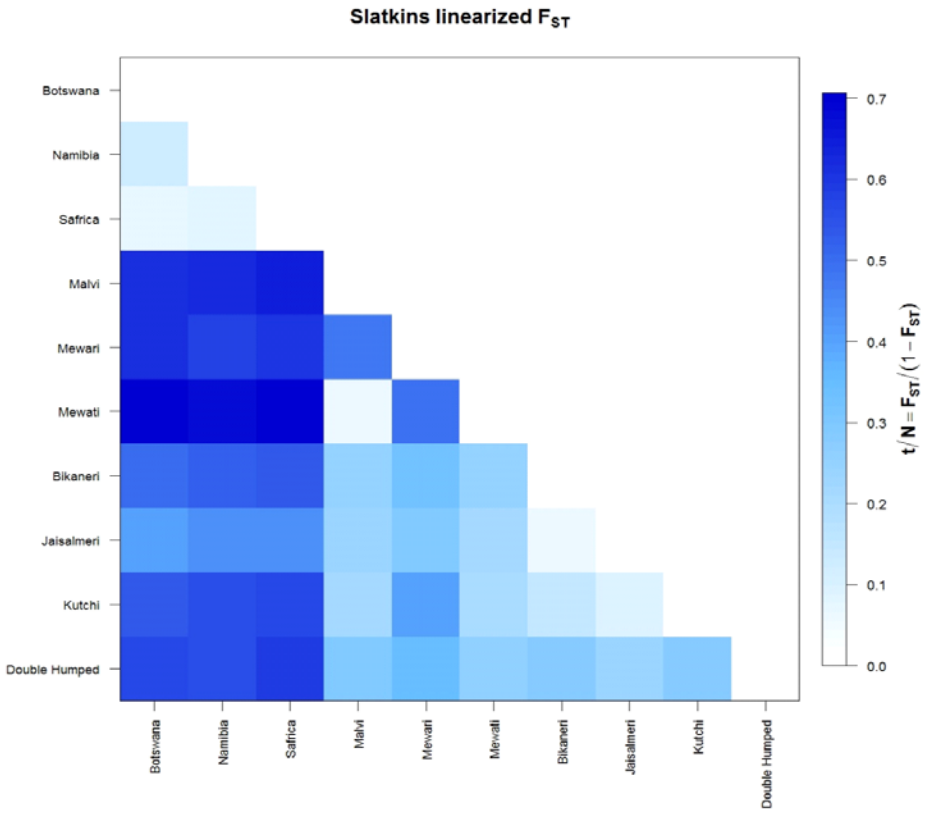

Fig. 4: Pairwise slatkin F_{ST} among breed/populations

loci deviated from Hardy Weinberg Equilibrium. While in case of Indian dromedarian the deviations recorded were 10 loci in Malvi, 3 in Mewari, 7 in Mewati, 11 in Bikaneri, Jaisalmeri and Kutchhi and 10 out of 12 in case of double humped camel. The values which showed high level of significance ($p<0.01$) are being denoted in the Table 3.

The estimates of F statistics F_{IS}, F_{IT} and F_{ST} represents inbreeding at the loci, total inbreeding and population differentiation respectively for each locus. The F_{IS} values were also calculated for all the 10 populations and were found to be 0.143, 0.255, 0.313, 0.138, 0.098, 0.15725, 0.46631, 0.48355, 0.36838 and 0.28603 for Botswana, Namibia, South Africa, Malvi, Mewari, Mewati, Bikaneri, Jaisalmeri, Kutchi and Double humped camel, respectively. The F_{IS} values were positive which points to local inbreeding effects in each sampled camel populations. The calculated F_{ST} provides a measure of population differentiation among the populations and have been depicted in Table 4. Similarly Nei's genetic distances were estimated and are depicted in Table 4 (above diagonal). The Neighbour joining algorithm was used to construct tree (Saitou and Nei, 1987) with bootstrapping over loci (Fig. 3). The FST values (Slatkin, 1995) among breeds/populations are depicted graphically in Fig. 4.

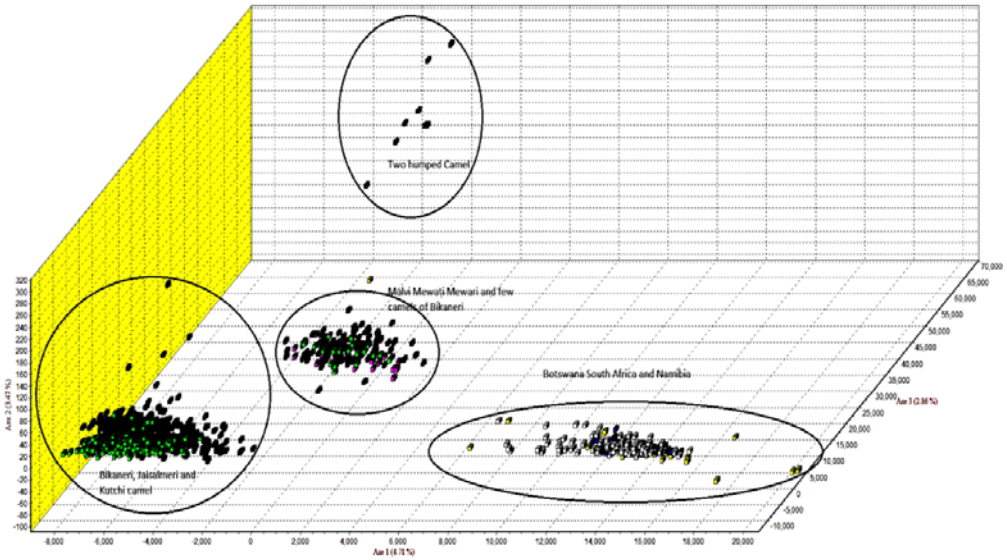

Fig. 5: Multivariate correspondence analysis of camel

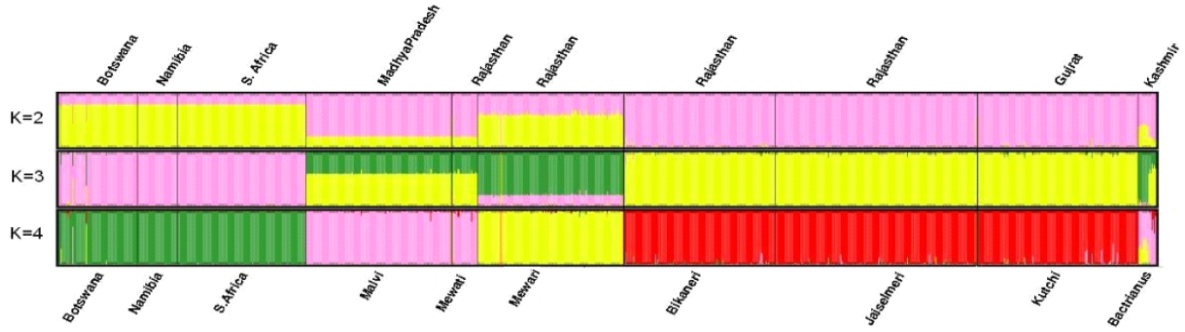

Fig. 6: Stacked vertical line plots of the estimated membership fractions of each individual analyzed for each of the k inferred clusters with k from 2 to 4, Individuals are grouped by population

Table 5: Estimated membership fractions of camel populations for each of the k inferred clusters with k from 2 to 4

	Number of inferred clusters								
	Two inferred clusters (K=2)		Three inferred clusters (K=3)			Four inferred clusters (K=4)			
Populations	1	2	1	2	3	1	2	3	4
Botswana	0.9780	0.0220	0.0160	0.9664	0.0176	0.0168	0.0120	0.9632	0.0080
Namibia	0.9976	0.0024	0.0014	0.9966	0.0020	0.0020	0.0010	0.9950	0.0020
SAfrica	0.9968	0.0032	0.0028	0.9944	0.0028	0.0030	0.0030	0.9918	0.0022
Malvi	0.0050	0.9950	0.6000	0.0038	0.3962	0.0030	0.9878	0.0030	0.0062
Mewari	0.4190	0.5810	0.0106	0.1988	0.7906	0.9812	0.0030	0.0088	0.0070
Mewati	0.0080	0.9920	0.6136	0.0024	0.3840	0.0030	0.9694	0.0030	0.0246
Bikaneri	0.2486	0.7514	0.7666	0.0500	0.1833	0.2270	0.0080	0.0070	0.7580
Jaisalmeri	0.2400	0.760.8	0.5600	0.0412	0.1532	0.1892	0.0070	0.0052	0.7986
Kutchi	0.2242	0.7758	0.8646	0.0266	0.1088	0.1301	0.0156	0.0020	0.8523
Bactrian camel	0.1414	0.8586	0.2967	0.0308	0.6725	0.2164	0.7184	0.0020	0.0632

The hierarchical Analysis of Molecular variance (AMOVA) revealed among groups component as 22.93%. Among populations within group contributed 11.31% to the total variance while the rest was accounted for by within population component. Thus the overall F_{ST} value was 0.34 which was highly significant ($p<0.001$). The values of effective number of migrants were high among the African populations. The values between Botswana

and Namibia, Botswana and South Africa and Namibia and South Africa were 4.04, 6.49 and 5.99, respectively. This depicts large gene flow among the dromedarian camel of South Africa, Botswana and Namibia and there was no significant population structuring and populations were homogenous (Nolte, 2005). All the Indian dromedarian cluster together while the Bactrian camel came out as an out-group as expected. However the Bactrian camel showed closer relationship with Indian dromedary which may be due to geographical proximity between the sampling areas of dromedarian and Bactrian camel.

The multivariate Correspondence analysis grouped the camel populations into four distinctive clusters. The first cluster of African Camel, the second of bactrian camel (out-group), the third cluster of camels belonging to Mewati, Mewari and Malvi camel while the fourth cluster grouped rest of the three populations. The first three axis of the correspondence analysis contribute

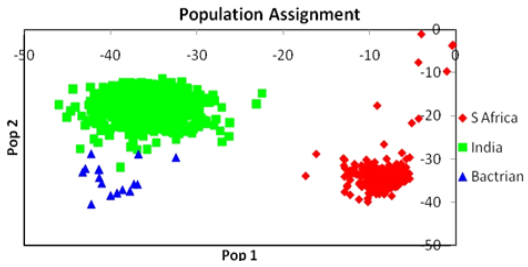

Fig. 7: Population assignment using log likelihood ratio

34.12, 19.81 and 18.98%, respectively. The relationship among the populations is depicted in Fig. 5.

The model-based clustering of the camel microsatellite allele frequencies showed that the likelihood of the model increases with the number of inferred clusters (k) and reaches a plateau around k = 4. The information contained in Table 5 represents percentage of the genome that is assigned to the inferred clusters in each model.

According to the results obtained, the genetic proximity among all the African camels i.e, Botswana, Namibia and South Africa is clearly visible (Fig. 6 and Table 5). At K = 2, the African camels show some proximity with the Mewari camels of Rajasthan. However at K = 3, significant differences are reflected between the African and Indian populations. At K = 4, four clusters are formed in which visible demarcation is depicted between African and Indian camels. The Indian camels are further clustered into 3 different groups, one group comprising of Malvi and Mewati, other cluster of Mewari, the next cluster had Bikaner, Jasialmeri and Kutchi. The bactrianus camel clearly differentiates itself from all other camels as shown in the Fig. 5. The individual assignment on the basis of negative log likelihood revealed three distinctive clusters of South African camels, Indian dromedary and bactrian camel as shown in Fig. 7. The inter-individual distances were estimated using Nei's genetic distance and Neighbour joining tree grouped the camels into four distinctive populations and have been depicted in Fig. 8.

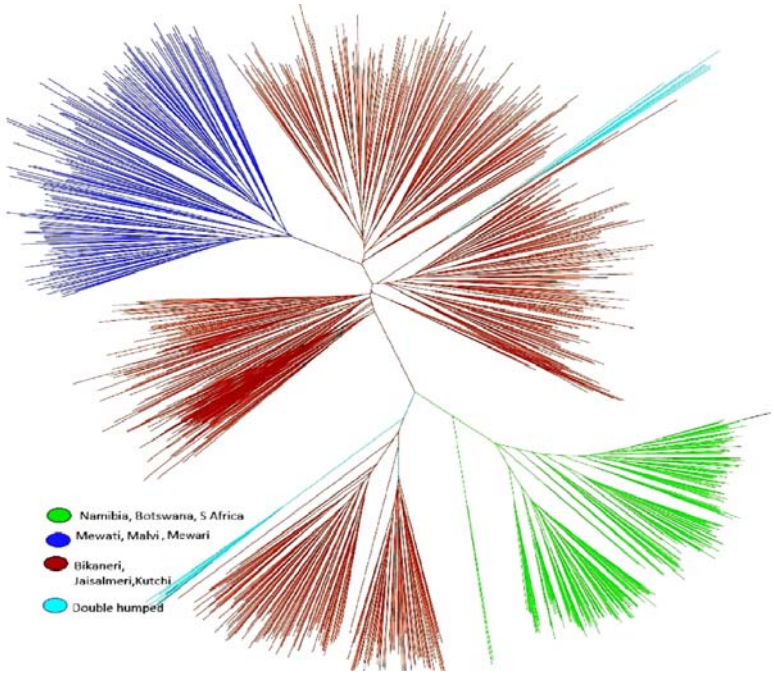

Fig. 8: Inter-individual based neighbor joining (NJ) tree utilizing nei's standard genetic distance

DISCUSSION

Among the 12 loci selected for the present study (Nolte, 2005), 7 loci were common with the study on Majorero camel (Schulz *et al*., 2005) and Kenyan camel (Schulz, 2010), 11 loci were common with Australian camel (Spencer and Woolnough, 2010), 8 with Canarian camel (Schulz, 2010).

The dromedary camel is found in the deserts of India (Thar Desert) at one end, countries of Central Asia and North Africa (Morocco, Tunisia, Algeria, Libysa and Egypt) in the West, migrant populations of dromedarian camel are found in Spain (Majorero and Canary islands), Australia, South Africa, Botswana and Namibia. There are relatively few microsatellite markers available for the dromedarian camel. Most of the camel populations have been studied with markers ranging from 3 to 23 loci (Vijh *et al*., 2007), while most of the studies have been undertaken with 10-15 microsatellite loci. In the present study, data was generated on those 12 microsatellite loci data of which was available for South Africa, Botswana and Namibia populations (Nolte, 2005). As India represents the Eastern most geographical location for the dromedary camel and South African region represents the farthest most area inhabited by camel, the differences between the two populations assume importance. Several studies have already been reported between these two extreme geographical areas of camel habitation. Among the migrant population of camel, Spencer and Woolnough (2010) reported very little genetic differentiation in Australian dromedary. Similar results were obtained for camels of South Africa, Botswana and Namibia (Nolte, 2005). The camel population of Europe especially of Canary islands and Majorero of Spain have been reported to have close proximity to North African camels (Schulz *et al*., 2005; Schulz, 2010) They reported only 3.1% differentiation between Majorero and African camel.

Mburu *et al*. (2003) reported that Kenyan population of camel are also poorly differentiated (F_{ST} = 0.009) and ruled out the classification of camels into distinct breeds based on socio- geographical criterion. The differentiation between Kenyan and non-Kenyan population based on 14 microsatellite loci was 5.6%. The non-Kenyan population included Pakistan, S. Arabia and UAE.

Most of the camel populations were poorly differentiated as they inhabited very similar environments, virtually negligible selection pressures and large migrations as most of the camel breeders were themselves nomadic.

Model based analysis of various populations by (Schulz, 2010) revealed similarity between Pakistan and UAE dromedary population and they share a common ancestry. Some ancestry is also shared by of Saudi Arabia camels also share the same ancestory. The Somalia, Rendille, Turkana and Gabbra form another group of camels and share a common ancestry.

The dromedary of India is likely to be genetically very similar to Pakistani camel owing to geographical contiguity and large migration of camel between the two countries (till a decade ago). However the dromedary of India is very well differentiated into the two distinctive camels: the lowland camel and hill camel. The Bactrian camel which has been taken as an out-group in the present study shared ancestry with the hill type camel. However the desert camels of India were not distinctively differentiated into well defined breeds (Vijh *et al*., 2007) as is the case with several other desert camel populations.

CONCLUSION

The present study reveals that the camel populations are not very much differentiated in African continent but the differentiation increases eastwardly and attains maximal differentiation in Indian subcontinent. This may be attributed to specialized utility selection, baggage/riding type camels and also due to their habitat (mountainous region). This has led to increased variability and existence of biodiversity in the region. It is expected that Indian camel population shall further get differentiated as its specialized usage shall increase leading to selection pressures for various economic traits (meat, milk, carting etc).

ACKNOWLEDGMENT

The study was funded by Indian Council of Agricultural Research grant C 30033 under National Agricultural Innovative Project Component IV, Basic and Strategic Research which is gratefully acknowledged.

REFERENCES

Ahmed, M.O., F.B. Salem, S. Bedhiaf, B. Rekik and M. Djemali, 2010. Genetic diversity in Tunisian dromedary (*Camelus dromedarius*) populations using microsatellite markers. Livest. Sci., 132: 182-185.

Al-Swailem, A.M., M.M. Shehata, A. Al-Busadahk, M.H. Fallatah and E. Askari, 2009. Evaluation of the genetic variability of microsatellite markers in Saudi Arabian camels. J. Food Agric. Environ., 7: 636-639.

Belkhir, K., P. Borsa, L. Chikhi, N. Raufaste and F. Bonhomme, 2004. GENETIX 4.05, Logiciel Sous Windows Tm Pour La Génétique Des Populations. Laboratoire Génome, Populations, Interactions, CNRS UMR 5000, Université de Montpellier II, Montpellier (France).

Excoffier, L. and H.E.L. Lischer, 2010. Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under linux and windows. Molecul. Ecol. Res., 10: 564-567.

Langella, O., 1999. Populations, 1.2.30 Copyright (C). CNRS UPR9034.

Mburu, D.N., J.W. Ochieng, SG. Kuria, H. Jianlin, B. Kaufmann, J.E.O. Rege and O. Hanotte, 2003. Genetic diversity and relationships of indigenous Kenyan camel (*Camelus dromedarius*) populations: Implications for their classification. Anim. Genet., 34: 26-32.

Nolte, M., 2005. Genetic Characterisation of Camelus dromedarius in Southern Africa. Thesis at Rand Afrikaans University.

Peakall, R. and P.E. Smouse, 2006. GENALEX 6: Genetic analysis in excel. Population genetic software for teaching and research. Molecul. Ecol. Notes, 6: 288-295.

Pritchard, J.K., 2009. Structure Software Ver 2.3.3 Retrieved from: http://pritch.bsd.uchicago.edu/ structure.html.

Rambaut, A., 2010. Figtree Software. Ver 1.3.1. Retrieved from: http://tree.bio.ed.ac.uk/software/ figtree/.

Saitou, N. and M. Nei, 1987. The neighbor-joining method: A new method for reconstructing phylogenetic trees. Molecul. Biol. Evolut., 4: 406-425.

Schulz, U., 2010. Isabel tupac-yupanqui, amparo martínez, susy méndez, juan vicente delgado, mariano gomez, susana dunner and javier cannon, 2010. Canarian Camel Traditional Dromedary Populat., 2: 561-571.

Sambrook, J. and D.W. Russell, 2001. Molecular Cloning: A Laboratory Manual. 3rd Edn., Cold Spring Harbor Laboratory Press, NY.

Schulz, U., Y. Minguez, M.L. Checa, P. Garcia-Atance, S. Dunner, D. Garcia and J. Canon, 2005. The Majorero camel (*Camelus dromedarius*) breed. Anim. Genet. Res. Inf., 36: 61-72.

Slatkin, M., 1995. A measure of population subdivision based on microsatellite allele frequencies. Genetics, 139: 457-462.

Spencer, P.B.S and A.P. Woolnough, 2010. Assessment and genetic characterisation of Australian camels using microsatellite polymorphisms. Livest. Sci., 129: 241-245.

Vijh, R.K., M.S. Tantia, B. Mishra and S.T.B. Kumar, 2007. Genetic diversity and differentiation of dromedarian camel of India. Anim. Biotechnol., 18: 81-90.

Yeh, F., C. Boyle, T. Rongcai, Z.Y. Ye and J.M. Xian, 1999. POPGENE: Ver 1.31. A Microsoft Window Based Freeware for Population Genetic Anaylsis, University of Alberta, Edmonton. Retrieved from: http:// ww.ualberta. a/-fyeh/fye.